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1646

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#4

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/659,860A

DATE: 12/26/2000
 TIME: 22:26:17

Input Set : A:\RTS-201.txt
 Output Set: N:\CRF3\12262000\I659860A.raw

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ENTERED

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3 <110> APPLICANT: Hong Zhang
4   Andrew T. Watt
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 7 EXPRESSION
8 <130> FILE REFERENCE: RTS-0201
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/659,860A
C--> 10 <141> CURRENT FILING DATE: 2000-09-11
10 <160> NUMBER OF SEQ ID NOS: 174
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Antisense Oligonucleotide
21 <400> SEQUENCE: 1
22 tccgtcatcg ctctcaggg
25 <210> SEQ ID NO: 2
26 <211> LENGTH: 20
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 2
34 atgcattctg cccccaagga
37 <210> SEQ ID NO: 3
38 <211> LENGTH: 2309
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (44)...(955)
46 <400> SEQUENCE: 3
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48                                     Met Ala Asp Asp
49                                     1
51 cag ggc tgt att gaa gag cag qgg gtt gag gat tca gca aat gaa gat
52 Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser Ala Asn Glu Asp
53 5      10      15      20
55 tca gtg gat gct aag cca gac cgg tcc tgg ttt gta ccg tcc ctc ttc
56 Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val Pro Ser Leu Phe
57      25      30      35
59 agt aag aag aag aaa aat gtc acc atg cga tcc atc aag acc acc cgg
60 Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr Arg
61      40      45      50
63 gac cga gtg cct aca tat cag tac aac atg aat ttt gaa aag ctg ggc
64 Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly
65      55      60      65
67 aaa tgc atc ata ala aac aac aag aac ttt gat aaa gtg aca ggt atg

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68 Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met
69      70      75      80
71 ggc gtt cga aac gga aca gac aaa gat gcc gag gcg ctc ttc aag tgc 343
72 Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys
73 85      90      95
75 ttc cga agc ctg ggt ttt gac gtg att gtc tat aat gac tgc tct tgc 391
76 Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys
77      105      110      115
79 gcc aag atg caa gat ctg ctt aaa aaa gct tct gaa gag gac cat aca 439
80 Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu Asp His Thr
81      120      125      130
83 aat gcc gcc tgc ttc gcc tgc atc ctc tta agc cat gga gaa gaa aat 487
84 Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn
85      135      140      145
87 gta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg aca gcc 535
88 Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala
89      150      155      160
91 cae ttt agg ggg gat aga tgc aaa acc ctt tta gag aaa ccc aaa ctc 583
92 His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Gln Lys Pro Lys Leu
93 165      170      175      180
95 ttc ttc att cag gct tgc cga ggg acc gag ctt gat gat gcc atc cag 631
96 Phe Phe Ile Gln Ala Cys Arg Gly Thr Gln Leu Asp Asp Gly Ile Gln
97      185      190      195
99 gcc gac tgc ggg ccc atc aat gac aca gal gct aat cct cga tac aag 679
100 Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn Pro Arg Tyr Lys
101      200      205      210
103 atc cca tgc gaa gct gac ttc ctc ttc gcc tat tcc acg gtt cca ggc 727
104 Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser Thr Val Pro Gly
105      215      220      225
107 tat tac tgc tgg agg agc cca gga aga ggc tcc tgg ttt gtg caa gcc 775
108 Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val Gln Ala
109      230      235      240
111 ctc tgc tcc atc ctg gag gag cac gga aaa gac ctg gaa atc atg cag 823
112 Leu Cys Ser Ile Leu Glu Gln His Gly Lys Asp Leu Glu Ile Met Gln
113 245      250      255      260
115 atc ctc acc agg gtg aat gac aga gtt gcc agg cac ttt gag tct cag 871
116 Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln
117      265      270      275
119 tct gat gac cca cac ttc cat gag aag aag cag atc ccc tgc gtg gtc 919
120 Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val
121      280      285      290
123 tcc atg ctc acc aag gaa ctc tac ttc agt caa tag ccatatcagg 965
124 Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
125      295      300
127 gglacattct agctgagaag caatgggtca ctcatlaatg aatcacattt tttlatgctc 1025
129 ttgaaatatt cagaaattct craggatttt aatttcagga aaatgtattg attcaacagg 1085
131 gaagaaactt tctgggtctg tcttttcttc tctgaatttt cagagacttt tttataatgt 1145
133 tattcatttg gtgactgtgt aactttctct taagattaat tttctcttctg tatgtctgtt 1205
135 accttgltta tagacttaat acatgcaaca gaagtgaact ctggagaaag ctcatggctg 1265

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TECH CENTER 1600/2200

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137 tgtccactgc aatttggtggt aacagtggta gagtcatgtt. tgcacttggc aaaaagaatc 1325
139 ccaatgtttg acaaaacaca gccaaagggga tatttactgc tctttattgc agantgtggg 1385
141 tattgagtgt gatttgaatg atttttcatt qctttaaggc agattttcat gcaaaaattc 1445
143 tcatatgagt tagagqagaa aaagcttaat gatctgata tctatccate aggatccagt 1505
145 ctggaaaaaca gaaccatttc taggtgtttc aacagagggg gtttaataca ggaattqac 1565
147 ttacatagat gataaaagag aagccaaaca gcaagaagct gtlaccacac ccagggtcat 1625
149 qaqqataatg qgaagaagtt tggtttctct tctccagtac tggggtcctc caggggagct 1685
151 qgaacatggt tgggggctgc ctagtgggag ttaggaccac caatggaltg tggaaaaagg 1745
153 agccatqaca agaacaagc cactgactga gatggagtga gctgagacag ataaagagaat 1805
155 accttgcttc acctatctg cctccacatc ttcaccacgc accttactgc ccaggcccat 1865
157 ctggaaqcca cctcaccaag gaccttggaa gagcaaggga cagtgaagca ggaqaagaac 1925
159 aagaaatgga tgaagcctg qcccataatg tgaacataag taatcactaa tgcacaacaa 1985
161 ttatccattt caatcattta ttcattgggt tctcagatag tctatgtatg tgtaaaaaaa 2045
163 tctgttttgg ctttatgtgc aaaatctgtt atagctttaa aalatatctg gaacttttta 2105
165 gattlatcca agccttattt tgaataaata tttgttactt ttagttctat aagtgaagaa 2165
167 gaatttatgg caaagatttt tggcactttg ttctcaagat ggtgttatct tttgaattct 2225
169 tgataaatga ctgttttttt ctgcctaata gtaactgggt aaaaaacaaa tgttcattat 2285
171 tatlgattaa aaatgtggtt gctt
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 26
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: PCR Primer
182 <400> SEQUENCE: 4
183 attggtgata acagtggtag agtcat. 26
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 20
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Primer
194 <400> SEQUENCE: 5
195 ccttggtgctg tgttttgtca
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 27
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR Probe
206 <400> SEQUENCE: 6
207 ttgcacttgg caaaaagaat cccaatg 27
210 <210> SEQ ID NO: 7
211 <211> LENGTH: 21
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: PCR Primer
218 <400> SEQUENCE: 7

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RAW SEQUENCE LISTING DATE: 12/26/2000
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219 caacggattt gtegtattg g
222 <210> SEQ ID NO: 8
223 <211> LENGTH: 26
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 8
231 ggcacacaa tccactttac cagagt
234 <210> SEQ ID NO: 9
235 <211> LENGTH: 21
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Probe
242 <400> SEQUENCE: 9
243 cgcctggtca ccagggtgc t
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 2006
248 <212> TYPE: DNA
249 <213> ORGANISM: Mus musculus
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (474)...(1496)
255 <400> SEQUENCE: 10
256 agctcagtga gctcgtatgt tactgcacat ttacacacac aatcacagga atttccatac
258 atgaataaaa accacacaaa tacatgtaga attggcaggt ggaacagagc cagcaagggc
260 tcaaaactaat caactcacttt cctcttccag catagtccaa ccaacagtag cacactttca
262 cctacaaate ttacagtagc tccatcaaat ctgcagtttt cacattattg aaatgtctg
264 ccacataaggt acaaattttag aatcaccaca ttatattaca tggctattct aggtcateta
266 tagatcaqat ccttaactac agtgattgaa gttcttcgta cagccatcaa aaaggagcac
268 atgacattta cctacttcta gctcacatct aaaggcatga aaagggttcc tttttttcaa
270 ctgacccaaa caetttaacc caatagtygc aggttccctc tctgtgtgtt tga atg
271 Met
272 1
274 ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg
275 Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
276 5 10 15
278 ccc tgc acc ctt gcg gag gac gga cgc tgc cgt ggc ctc ctc gcc gcc
279 Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
280 20 25 30
282 gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa
283 Ala Val Gly Thr Met Thr Asp Asp Glu Asp Cys Ala Ala Glu Leu Glu
284 35 40 45
286 aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc
287 Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg
288 50 55 60 65
290 tcc tct atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct
291 Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser

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292		70		75		80	
294	gag ggc ccc gtc agg acc ggc cgg gac cga glg ccc act tat ctg tac						764
295	Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr						
296		85		90		95	
298	cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag						812
299	Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys						
300		100		105		110	
302	aac ttc gac aaa cgc aca ggt atg gac gtc cgg aat ggg acg gac aaa						860
303	Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys						
304		115		120		125	
306	gat gca ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta						908
307	Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val						
308	130		135		140		145
310	acc gtc cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aqa						956
311	Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg						
312		150		155		160	
314	aaa gcc tct gag gag gac cac agc aac tgg gcc tgc ttc gcc tgc gtc						1004
315	Lys Ala Ser Glu Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val						
316		165		170		175	
318	ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg						1052
319	Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val						
320		180		185		190	
322	aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa						1100
323	Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys						
324		195		200		205	
326	acc ctg tta gag aaa ccc aaa ctc ttc ttc att cag gca tgc cga ggg						1148
327	Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly						
328	210		215		220		225
330	acg gag ctc gac gat gga atc cag gct gac tgg ggg ccc atc aac gac						1196
331	Thr Glu Leu Asp Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp						
332		230		235		240	
334	att gac gct aat ccc cgc aac aag atc ccg gtg gaa gcc gac ttc ctc						1244
335	Ile Asp Ala Asn Pro Arg Asn Lys Ile Pro Val Glu Ala Asp Phe Leu						
336		245		250		255	
338	ttt gct tac tcc acg gtl cca ggt tal tac tca tgg agg aac cca ggg						1292
339	Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly						
340		260		265		270	
342	aaa ggc tcc tgg ttt gty cag gcc ctc tgc tcc atc ctg aat gag cat						1310
343	Lys Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu Asn Glu His						
344		275		280		285	
346	gac aag gac ctc gag atc atg caa atc ctg acc agg gtg aac gac agg						1388
347	Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg						
348	290		295		300		305
350	gtg gcc agg cac ttc gag tcc cag tct gat gal cca cgc ttc aac gag						1436
351	Val Ala Arg His Phe Glu Ser Gln Ser Asp Asp Pro Arg Phe Asn Glu						
352		310		315		320	
354	aag aag caa atc ccg tgt atg gtg tcc atg ctc acc aaa gag ctg tac						1484
355	Lys Lys Gln Ile Pro Cys Met Val Ser Met Leu Thr Lys Glu Leu Tyr						
356		325		330		335	

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date